

SEQUENCE LISTING

<110> Board of Control of Michigan Technological Univers

<120> METHOD FOR ENHANCING CELLULOSE AND MODIFYING LIGNIN
BIOSYNTHESIS IN PLANTS

<130> 66040/9675

<140>

<141>

<150> 60/135,280

<151> 1999-05-21

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 3232

<212> DNA

<213> Populus tremuloides

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<221> CDS

<222> (69)..(3002)

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cag	gtg	ggg	cat	gat	gca	aat	ggg	gag	cta	ttt	gtg	gct	tgc	cat	gag	158
Gln	Val	Gly	His	Asp	Ala	Asn	Gly	Glu	Leu	Phe	Val	Ala	Cys	His	Glu	
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tgt	agc	tat	ccc	atg	tgc	aag	tct	tgt	ttc	gag	ttt	gaa	atc	aat	gag	206
Cys	Ser	Tyr	Pro	Met	Cys	Lys	Ser	Cys	Phe	Glu	Phe	Glu	Ile	Asn	Glu	
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Gly	Arg	Lys	Val	Cys	Leu	Arg	Cys	Gly	Ser	Pro	Tyr	Asp	Glu	Asn	Leu	
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Leu	Asp	Asp	Val	Glu	Lys	Lys	Gly	Ser	Gly	Asn	Gln	Ser	Thr	Met	Ala	
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tct	cac	ctc	aac	gat	tct	cag	gat	gtc	gga	atc	cat	gct	aga	cat	atc	350
Ser	His	Leu	Asn	Asp	Ser	Gln	Asp	Val	Gly	Ile	His	Ala	Arg	His	Ile	
		80				85					90					

agt	agt	gtg	tcc	act	gtg	gat	agt	gaa	atg	aat	gat	gaa	tat	ggg	aat	398
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Pro Ile Trp Lys Asn Arg Val Lys Ser Cys Lys Asp Lys Glu Asn Lys	115	120	125	
aag aaa aag aga agt cct aag gct gaa act gaa cca gct caa gtt cct				494
Lys Lys Lys Arg Ser Pro Lys Ala Glu Thr Glu Pro Ala Gln Val Pro	130	135	140	
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Thr Glu Gln Gln Met Glu Glu Lys Pro Ser Ala Glu Ala Ser Glu Pro	145	150	155	
ctt tca att gtt tat cca att cca cgc aac aag ctc aca cca tac aga				590
Leu Ser Ile Val Tyr Pro Ile Pro Arg Asn Lys Leu Thr Pro Tyr Arg	160	165	170	
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Ala Val Ile Ile Met Arg Leu Val Ile Leu Gly Leu Phe Phe His Phe	175	180	185	190
aga ata aca aat cct gtc gat agt gcc ttt ggc ctg tgg ctt act tct				686
Arg Ile Thr Asn Pro Val Asp Ser Ala Phe Gly Leu Trp Leu Thr Ser	195	200	205	
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Pro Lys Trp Asn Pro Val Asn Arg Glu Thr Tyr Ile Glu Arg Leu Ser	225	230	235	
gca agg tat gaa aga gag ggt gag cct tct cag ctt gct ggt gtg gat				830
Ala Arg Tyr Glu Arg Glu Gly Glu Pro Ser Gln Leu Ala Gly Val Asp	240	245	250	
ttt ttc gtg agt act gtt gat ccg ctg aag gaa ccg cca ttg atc act				878
Phe Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr	255	260	265	270
gcc aat aca gtc ctt tcc atc ctt gct gtg gac tat ccc gtc gat aaa				926
Ala Asn Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys	275	280	285	
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Val Ser Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Ser Phe Glu	290	295	300	
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Ser Leu Val Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys	305	310	315	
aaa aaa ttc tca att gaa cca aga gca ccg gag ttt tac ttc tca cag				1070
Lys Lys Phe Ser Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ser Gln	320	325	330	

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gcc ctg gta gca aag gct cag aaa aca cct gaa gaa gga tgg act atg Ala Leu Val Ala Lys Ala Gln Lys Thr Pro Glu Glu Gly Trp Thr Met 370 375 380	1214
caa gat gga aca cct tgg cct ggg aat aac aca cgt gat cac cct ggg Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Thr Arg Asp His Pro Gly 385 390 395	1262
cat gat tca ggt ctt cct tgg gaa ata ctg gga gct cgt gac att gaa His Asp Ser Gly Leu Pro Trp Glu Ile Leu Gly Ala Arg Asp Ile Glu 400 405 410	1310
gga aat gaa cta cct cgt cta gta tat gtc tcc agg gag aag aga cct Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro 415 420 425 430	1358
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gat cac tat gta aac aat agc aag gct gtt cga gag gca atg tgc atc Asp His Tyr Val Asn Asn Ser Lys Ala Val Arg Glu Ala Met Cys Ile 465 470 475	1502
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575 580 585 590	
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595 600 605	
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Ser Val Phe Ile Glu Ser Thr Leu Met Glu Asn Gly Gly Val Pro Glu	
625 630 635	
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Ser Ala Asn Ser Pro Pro Phe Ile Lys Glu Ala Ile Gln Val Ile Gly	
640 645 650	
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Cys Gly Tyr Glu Glu Lys Thr Glu Trp Gly Lys Gln Ile Gly Trp Ile	
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tat ggg tca gtc act gag gat atc tta agt ggc ttc aag atg cac tgc	2126
Tyr Gly Ser Val Thr Glu Asp Ile Leu Ser Gly Phe Lys Met His Cys	
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Arg Gly Trp Arg Ser Ile Tyr Cys Met Pro Val Arg Pro Ala Phe Lys	
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Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu His Gln Val Leu Arg	
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Trp Ala Leu Gly Ser Val Glu Ile Phe Phe Ser Arg His Cys Pro Leu	
720 725 730	
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Trp Tyr Gly Phe Gly Gly Gly Arg Leu Lys Trp Leu Gln Arg Leu Ala	
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tat ata aac acc att gtg tac cca ttt aca tcc ctc cct ctc att gcc	2366
Tyr Ile Asn Thr Ile Val Tyr Pro Phe Thr Ser Leu Pro Leu Ile Ala	
755 760 765	
tat tgc aca att cct gca gtt tgt ctg ctc acc gga aaa ttc atc ata	2414
Tyr Cys Thr Ile Pro Ala Val Cys Leu Leu Thr Gly Lys Phe Ile Ile	
770 775 780	
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Pro Thr Leu Ser Asn Leu Ala Ser Met Leu Phe Leu Gly Leu Phe Ile
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Ser Ile Ile Val Thr Ala Val Leu Glu Leu Arg Trp Ser Gly Val Ser
800 805 810

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Ile Glu Asp Leu Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Val
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tca gcc cat ctc ttt gcg gtc ttc cag gga ttc tta aaa atg ttg gct 2606
Ser Ala His Leu Phe Ala Val Phe Gln Gly Phe Leu Lys Met Leu Ala
835 840 845

ggc atc gat acg aac ttc act gtc aca gca aaa gca gcc gaa gat gca 2654
Gly Ile Asp Thr Asn Phe Thr Val Thr Ala Lys Ala Ala Glu Asp Ala
850 855 860

gaa ttt ggg gag cta tat atg gtc aag tgg aca aca ctt ttg att cct 2702
Glu Phe Gly Glu Leu Tyr Met Val Lys Trp Thr Thr Leu Leu Ile Pro
865 870 875

cca acc aca ctt ctc att atc aat atg tcg ggt tgt gct gga ttc tct 2750
Pro Thr Thr Leu Leu Ile Ile Asn Met Ser Gly Cys Ala Gly Phe Ser
880 885 890

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Asp Ala Leu Asn Lys Gly Tyr Glu Ala Trp Gly Pro Leu Phe Gly Lys
895 900 905 910

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Val Phe Phe Ala Phe Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys
915 920 925

ggt cta atg ggt cgc caa aac cta aca cca acc att gtt gtt ctc tgg 2894
Gly Leu Met Gly Arg Gln Asn Leu Thr Pro Thr Ile Val Val Leu Trp
930 935 940

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Ser Val Leu Leu Ala Ser Val Phe Ser Leu Val Trp Val Lys Ile Asn
945 950 955

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Ser Ile Asp Cys
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tcgctgtcag tatttaaagt aactgcaaga tgattgttct ctatgaagtt ttgaacagtt 3162

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 Asp Val Glu Lys Lys Gly Ser Gly Asn Gln Ser Thr Met Ala -
 65 70 75
 Leu Asn Asp Ser Gln Asp Val Gly Ile His Ala Arg His Ile -
 85 90
 Val Ser Thr Val Asp Ser Glu Met Asn Asp Glu Tyr Gly Asn -
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 Trp Lys Asn Arg Val Lys Ser Cys Lys Asp Lys Glu Asn Lys -
 115 120 125
 Lys Arg Ser Pro Lys Ala Glu Thr Glu Pro Ala Gln Val Pro -
 130 135 140
 Gln Gln Met Glu Glu Lys Pro Ser Ala Glu Ala Ser Glu Pro -
 145 150 155
 Ile Val Tyr Pro Ile Pro Arg Asn Lys Leu Thr Pro Tyr Arg -
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 Ile Ile Met Arg Leu Val Ile Leu Gly Leu Phe Phe His Phe -
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 Thr Asn Pro Val Asp Ser Ala Phe Gly Leu Trp Leu Thr Ser -
 195 200 205
 Cys Glu Ile Trp Phe Ala Phe Ser Trp Val Leu Asp Gln Phe -
 210 215 220
 Trp Asn Pro Val Asn Arg Glu Thr Tyr Ile Glu Arg Leu Ser -
 225 230 235
 Tyr Glu Arg Glu Gly Glu Pro Ser Gln Leu Ala Gly Val Asp -
 245 250

Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Ile Thr Ala Asn
 260 265 270
 Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys Val Ser
 275 280 285
 Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Ser Phe Glu Ser Leu
 290 295 300
 Val Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys
 305 310 315 320
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 Asp Tyr Leu Lys Asp Lys Val Gln Pro Ser Phe Val Lys Glu Arg Arg
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 Ala Met Lys Arg Asp Tyr Glu Glu Tyr Lys Val Arg Val Asn Ala Leu
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 370 375 380
 Gly Thr Pro Trp Pro Gly Asn Asn Thr Arg Asp His Pro Gly His Asp
 385 390 395 400
 Ser Gly Leu Pro Trp Glu Ile Leu Gly Ala Arg Asp Ile Glu Gly Asn
 405 410 415
 Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr
 420 425 430
 Gln His His Lys Lys Ala Gly Ala Glu Asn Ala Leu Val Arg Val Ser
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 Ala Val Leu Thr Asn Ala Pro Tyr Ile Leu Asn Val Asp Cys Asp His
 450 455 460
 Tyr Val Asn Asn Ser Lys Ala Val Arg Glu Ala Met Cys Ile Leu Met
 465 470 475 480
 Asp Pro Gln Val Gly Arg Asp Val Cys Tyr Val Gln Phe Pro Gln Arg
 485 490 495
 Phe Asp Gly Ile Asp Lys Ser Asp Arg Tyr Ala Asn Arg Asn Val Val
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Cys Phe Ser Cys Cys Cys Pro Ser Lys Lys Lys Pro Ala Gln Asp Pro
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 Asn Ser Pro Pro Phe Ile Lys Glu Ala Ile Gln Val Ile Gly Cys Gly
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 Tyr Glu Glu Lys Thr Glu Trp Gly Lys Gln Ile Gly Trp Ile Tyr Gly
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 Ser Val Thr Glu Asp Ile Leu Ser Gly Phe Lys Met His Cys Arg Gly
 675 680 685
 Trp Arg Ser Ile Tyr Cys Met Pro Val Arg Pro Ala Phe Lys Gly Ser
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 Ala Pro Ile Asn Leu Ser Asp Arg Leu His Gln Val Leu Arg Trp Ala
 705 710 715 720
 Leu Gly Ser Val Glu Ile Phe Phe Ser Arg His Cys Pro Leu Trp Tyr
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 Gly Phe Gly Gly Gly Arg Leu Lys Trp Leu Gln Arg Leu Ala Tyr Ile
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 Thr Ile Pro Ala Val Cys Leu Leu Thr Gly Lys Phe Ile Ile Pro Thr
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 His Leu Phe Ala Val Phe Gln Gly Phe Leu Lys Met Leu Ala Gly Ile
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 850 855 860

Gly Glu Leu Tyr Met Val Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr
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 Met Met Glu Ser Gly Ala Pro Ile Cys His Thr Cys Gly Glu Gln Val
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 ggg cat gat gca aat ggg gag cta ttt gtg gct tgc cat gag tgt agc 936
 Gly His Asp Ala Asn Gly Glu Leu Phe Val Ala Cys His Glu Cys Ser
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 tat ccc atg tgc aag tct tgt ttc gag ttt gaa atc aaa gag ggc cgg 984
 Tyr Pro Met Cys Lys Ser Cys Phe Glu Phe Glu Ile Lys Glu Gly Arg
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 <212> PRT
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 <223> 5' flanking region of PtCelA coding sequence

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 Pro Cys Tyr Glu Tyr Glu Arg Arg Glu Gly Asn Gln Ala Cys Pro Gln
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 Cys Lys Thr Arg Phe Lys Arg Leu Lys Gly Ser Pro Arg Val Glu Gly
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 Asp Glu Glu Glu Asp Asp Ile Asp Asp Leu Asp Asn Glu Phe Glu Tyr
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